P1. Relationship between rice genetic diversity and microbiota composition in traditional Yuanyang rice terraces of China.

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Rice has been annually cultivated for more than 1400 years in the Yuanyang terraces (YYT) of Yunnan, China. Interestingly, the level of diseases observed in this region has always remained low and, consequently, the YYT rice production has never been constrained by a heavy disease burden. A recent study has shown that the arsenal of resistance genes overall born by the rice traditional varieties that are grown in YYT prevents the dissemination of the highly virulent fungal pathogen *Magnaporthe oryzae* (Liao et al 2016). While the use of more than 40 traditional rice varieties has been maintained for centuries in YYT, but the use of a few modern improved varieties has been drastically increased the last few years. This significant change in the overall level of diversity of the rice varieties growing in YYT may affect the long-term sustainable rice protection of this region. Our overarching hypothesis is that the simplification of the varietal landscape is driving a modification of the YYT rice microbiota, which may by extension have an impact on the YYT plant pathogen dynamics, and further on the pathogen emergence or non-emergence. In this study, we have focused our sampling design on a YYT village where both traditional and modern varieties have been equally cultivated for 3-4 years. We have sampled 9 fields cultivated with traditional rice varieties and 9 fields cultivated with improved rice varieties. The 180 collected plants (10 plants X 18 fields) were genotyped after partial genome sequencing (genotyping-by-sequencing approach, GBS). The GBS library was established using the ApekI restriction enzyme, we genotyped the panel of samples with up to 5000 informative SNP markers. This GBS study has confirmed the high degree of diversity of YYT traditional rice varieties in comparison to the low level of diversity of the modern improved varieties that are increasingly introduced in the YYT region. We have further characterized the roots and the stem microbiota using the virion-associated nucleic acid metagenomics-based approach to characterize the virus communities and metabarcoding methods for the bacteria and fungi communities. Besides highlighting the characterization of the microbiota of each rice variety, we will present preliminary results on the relationship between the YYT host genetic diversity and the rice microbiota composition.

References

Liao, J., Huang, H., Meusnier, I., Adreit, H., Ducasse, A., Bonnot, F., Pan, L., He, X., Kroj, T., Fournier, E., Tharreau, D., Gladieux, P., and Morel, J.B. 2016. Pathogen effectors and plant immunity determine specialization of the blast fungus to rice subspecies. eLife 5: e19377.

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P2. Liver microbiome of *Peromyscus leucopus*, a key reservoir host species for emerging infectious diseases in North America.

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